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recovering a genetically altered plant from said plant cell, said genetically altered plant characterized by an altered nutritional profile relative to a wild-type of said plant.

Please cancel claim 39.

Please rewrite claim 40 as follows:

40. (Once amended) A method for altering a nutritional profile of a plant, comprising the steps of:

selecting a nucleic acid sequence for its ability to encode a protein capable of modifying the utilization of a substrate in the phenylpropanoid pathway of said plant, said protein being non-native to said phenylpropanoid pathway;

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transforming a plant cell of said plant with an expression cassette comprising said nucleic acid sequence, said plant being of a type used as an animal feed, with the proviso that said plant is not rice or *Arabidopsis*; and

recovering a genetically altered plant from said plant cell, said genetically altered plant characterized by an altered nutritional profile relative to a wild-type of said plant.

Please cancel claim 47.

Please rewrite claims 49-66 as follows:

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49. (Once amended) A genetically modified plant or a descendant thereof, said plant being of a type used as an animal feed, with the proviso that said plant is not rice or *Arabidopsis*, said plant comprising a recombinant nucleic acid sequence stably incorporated into the genome of said plant, said recombinant nucleic acid sequence encoding a protein which modifies the utilization of a substrate in the phenylpropanoid metabolic pathway of said plant, said protein being non-native to

said phenylpropanoid metabolic pathway, said plant having an improved nutritional profile relative to a wild-type of said plant.

50. (Once amended) The genetically modified plant or descendant thereof of claim 49, wherein said substrate is not a primary metabolite of the group selected from glucose, amino acids, common fatty acids and nucleotides.

51. (Once amended) The genetically modified plant or descendant thereof of claim 49, wherein said nucleic acid sequence is under the control of a tissue selective promoter.

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52. (Once amended) The genetically modified plant or descendant thereof of claim 51, wherein said promoter is seed selective.

53. (Once amended) The genetically modified plant or descendant thereof of claim 52, wherein said seed selective promoter is a phaseolin promoter or a napin promoter.

54. (Once amended) A plant cell, plant seed, plant component or plant progeny derived from the genetically modified plant of claim 49.

55. (Once amended) The genetically modified plant or descendant thereof of claim 49, wherein said encoded protein is a choline metabolizing enzyme.

56. (Once amended) The genetically modified plant or descendant thereof of claim 55, wherein said choline metabolizing enzyme is choline oxidase.

57. (Once amended) The genetically modified plant or descendant thereof of claim 56, wherein said nucleic acid sequence encoding said choline oxidase is under the control of a seed-selective promoter active in plant cells, and wherein said expression cassette further comprises a nucleic acid sequence that encodes a betaine aldehyde dehydrogenase capable of converting betaine aldehyde to betaine, said betaine aldehyde dehydrogenase encoding nucleic acid sequence being under the control of a seed-selective promoter active in plant cells.

58. (Once amended) The genetically modified plant or descendant thereof of claim 49, wherein said improved nutritional profile comprises an altered lignin content relative to said wild-type of said plant.
59. (Once amended) The genetically modified plant or descendant thereof of claim 49, wherein said improved nutritional profile comprises a reduced sinapine content relative to said wild-type of said plant.
60. (Once amended) The genetically modified plant or descendant thereof of claim 49, wherein said plant is a member of the Dicotyledoneae or Monocotyledoneae.
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61. (Once amended) The genetically modified plant or descendant thereof of claim 49, wherein said plant is a member of a family selected from the group consisting of Malvaceae, Linaceae, Compositae, Fabaceae, Euphorbiaceae, Gramineae and Oleaceae.
62. (Once amended) The genetically modified plant or descendant thereof of claim 49, wherein said plant is a member of the family Brassicaceae (= Cruciferae).
63. (Once amended) The genetically modified plant or descendant thereof of claim 49, wherein said plant is a member of a genus selected from the group consisting of *Linum*, *Gossypium*, *Glycine*, *Arachis*, *Carthamus*, *Helianthus*, *Medicago*, *Sinapis*, *Raphanus*, *Ricinus*, *Olea*, *Zea*, *Hordium*, and *Triticale*.
64. (Once amended) The genetically modified plant or descendant thereof of claim 49, wherein said plant is of the genus *Brassica*.
65. (Once amended) The genetically modified plant or descendant thereof of claim 49, wherein said plant is *Brassica napus* or *Brassica rapa*.
66. (Once amended) An animal feed derived at least in part from the genetically modified plant or descendant thereof of claim 49.

Please add the following new claims:

67. A method for altering a nutritional profile of a plant of the genus *Brassica*, comprising the steps of:

selecting a nucleic acid sequence for its ability to encode a protein capable of modifying the utilization of a substrate in a secondary metabolic pathway associated with a nutritional profile of a plant of the genus *Brassica*, said protein being non-native to said secondary metabolic pathway;

transforming a plant cell of said *Brassica* plant with an expression cassette comprising said nucleic acid sequence; and

recovering a genetically altered *Brassica* plant from said plant cell, said genetically altered plant characterized by an altered nutritional profile relative to a wild-type of said plant.

68. The method of claim 67, wherein said protein is a choline metabolizing enzyme and said secondary metabolic pathway is the phenylpropanoid pathway.

69. The method of claim 68, wherein said choline metabolizing enzyme is choline oxidase.

70. The method of claim 69, wherein said nucleic acid sequence is under the control of a seed specific promoter.

71. The method of claim 70, wherein said *Brassica* plant is *B. napus* or *B. rapa*.

72. A genetically modified plant of the genus *Brassica*, or a descendant thereof, said *Brassica* plant comprising a recombinant nucleic acid sequence stably incorporated into the genome of said *Brassica* plant, said recombinant nucleic acid sequence encoding a protein which modifies the utilization of a substrate in a secondary metabolic pathway associated with a nutritional profile of said *Brassica* plant, said protein being non-native to said secondary metabolic pathway, said

genetically modified *Brassica* plant having an improved nutritional profile relative to a wild-type of said plant.

73. The genetically modified *Brassica* plant or descendent thereof of claim 72, wherein said protein is a choline metabolizing enzyme and said secondary metabolic pathway is the phenylpropanoid pathway.

74. The genetically modified *Brassica* plant or descendent thereof of claim 73, wherein said choline metabolizing enzyme is choline oxidase.

75. The genetically modified *Brassica* plant or descendent thereof of claim 74, wherein said nucleic acid sequence is under the control of a seed specific promoter.

76. The genetically modified *Brassica* plant or descendent thereof of claim 75, wherein said *Brassica* plant is *B. napus* or *B. rapa*.

77. The method of claim 34 or 40, wherein said plant is a member of a family selected from the group consisting of Malvaceae, Linaceae, Compositae, Fabaceae, Euphorbiaceae, Gramineae and Oleaceae.

78. The method of claim 34 or 40, wherein said plant is a member of a genus selected from the group consisting of *Linum*, *Gossypium*, *Glycine*, *Arachis*, *Carthamus*, *Helianthus*, *Medicago*, *Sinapis*, *Raphanus*, *Ricinus*, *Olea*, *Zea*, *Hordium*, and *Triticale*.

79. The method of claim 34 or 40, wherein said plant is selected from the group consisting of soybean, cotton, sunflower, alfalfa, flax, sorghum, corn, wheat, barley and rye.

80. The genetically modified plant or descendant thereof of claim 49, wherein said plant is selected from the group consisting of soybean, cotton, sunflower, alfalfa, flax, sorghum, corn, wheat, barley and rye.